

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/525,019
Source: P4710
Date Processed by STIC: 9/1/05

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PCT

RAW SEQUENCE LISTING

DATE: 09/01/2005

PATENT APPLICATION: US/10/525,019

TIME: 15:47:04

Input Set : A:\GIES3002.ST25.txt

Output Set: N:\CRF4\09012005\J525019.raw

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3 <110> APPLICANT: Giesing, Michael
4   Suchy, Bernhard
6 <120> TITLE OF INVENTION: METHOD FOR ANALYZING BODY FLUIDS FOR THE PRESENCE OF CANCER
7   CELLS, USE THEREOF, CORRESPONDING ANALYSIS KITS, AND USE OF
8   SPECIFIC ACTIVE SUBSTANCES FOR TREATING CANCER
10 <130> FILE REFERENCE: GIES3002
12 <140> CURRENT APPLICATION NUMBER: 10/525,019
13 <141> CURRENT FILING DATE: 2005-02-18
15 <150> PRIOR APPLICATION NUMBER: PCT/EP03/009229
16 <151> PRIOR FILING DATE: 2003-08-20
18 <150> PRIOR APPLICATION NUMBER: DE 102 38 046.5
19 <151> PRIOR FILING DATE: 2002-08-20
21 <160> NUMBER OF SEQ ID NOS: 22
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 22
27 <212> TYPE: DNA
28 <213> ORGANISM: Artificial
30 <220> FEATURE:
31 <223> OTHER INFORMATION: forward primer (MNSOD)
33 <400> SEQUENCE: 1
34 gtcaccgagg agaagtacca gg                                22
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 20
39 <212> TYPE: DNA
40 <213> ORGANISM: Artificial
42 <220> FEATURE:
43 <223> OTHER INFORMATION: reverse primer (MNSOD)
45 <400> SEQUENCE: 2
46 gggctgaggt ttgtccagaa                                20
49 <210> SEQ ID NO: 3
50 <211> LENGTH: 27
51 <212> TYPE: DNA
52 <213> ORGANISM: Artificial
54 <220> FEATURE:
55 <223> OTHER INFORMATION: probe (MNSOD)
57 <400> SEQUENCE: 3
58 cggtggccaa gggagatggt acagccc                        27
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 23
63 <212> TYPE: DNA
64 <213> ORGANISM: Artificial
66 <220> FEATURE:

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67 <223> OTHER INFORMATION: forward primer (TXNRD1)
69 <400> SEQUENCE: 4
70 ggagggcaga cttcaaaagc tac                                     23
73 <210> SEQ ID NO: 5
74 <211> LENGTH: 22
75 <212> TYPE: DNA
76 <213> ORGANISM: Artificial
78 <220> FEATURE:
79 <223> OTHER INFORMATION: reverse primer (TXNRD1)
81 <400> SEQUENCE: 5
82 acaaagtcca ggaccatcac ct                                     22
85 <210> SEQ ID NO: 6
86 <211> LENGTH: 26
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: probe (TXNRD1)
93 <400> SEQUENCE: 6
94 ttgggctgcc tccttagcag ctgcca                                26
97 <210> SEQ ID NO: 7
98 <211> LENGTH: 17
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial
102 <220> FEATURE:
103 <223> OTHER INFORMATION: forward primer (GPX1)
105 <400> SEQUENCE: 7
106 ctcggcttcc cgtgcaa                                         17
109 <210> SEQ ID NO: 8
110 <211> LENGTH: 19
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial
114 <220> FEATURE:
115 <223> OTHER INFORMATION: reverse primer (GPX1)
117 <400> SEQUENCE: 8
118 tgaagttggg ctcgaaccc                                       19
121 <210> SEQ ID NO: 9
122 <211> LENGTH: 28
123 <212> TYPE: DNA
124 <213> ORGANISM: Artificial
126 <220> FEATURE:
127 <223> OTHER INFORMATION: probe (GPX1)
129 <400> SEQUENCE: 9
130 agtttgggca tcaggagaac gccaaagaa                            28
133 <210> SEQ ID NO: 10
134 <211> LENGTH: 19
135 <212> TYPE: DNA
136 <213> ORGANISM: Artificial
138 <220> FEATURE:
139 <223> OTHER INFORMATION: forward primer (GAPDH)

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141 <400> SEQUENCE: 10
142 tgctgatgcc cccatgttc                                     19
145 <210> SEQ ID NO: 11
146 <211> LENGTH: 20
147 <212> TYPE: DNA
148 <213> ORGANISM: Artificial
150 <220> FEATURE:
151 <223> OTHER INFORMATION: reverse primer (GAPDH)
153 <400> SEQUENCE: 11
154 ggcagtgatg gcatggactg                                     20
157 <210> SEQ ID NO: 12
158 <211> LENGTH: 27
159 <212> TYPE: DNA
160 <213> ORGANISM: Artificial
162 <220> FEATURE:
163 <223> OTHER INFORMATION: probe (GAPDH)
165 <400> SEQUENCE: 12
166 tcaagatcat cagcaatgcc tcctgca                             27
169 <210> SEQ ID NO: 13
170 <211> LENGTH: 222
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 13
176 Met Leu Ser Arg Ala Val Cys Gly Thr Ser Arg Gln Leu Ala Pro Ala
177 1          5          10          15
180 Leu Gly Tyr Leu Gly Ser Arg Gln Lys His Ser Leu Pro Asp Leu Pro
181          20          25          30
184 Tyr Asp Tyr Gly Ala Leu Glu Pro His Ile Asn Ala Gln Ile Met Gln
185          35          40          45
188 Leu His His Ser Lys His His Ala Ala Tyr Val Asn Asn Leu Asn Val
189          50          55          60
192 Thr Glu Glu Lys Tyr Gln Glu Ala Leu Ala Lys Gly Asp Val Thr Ala
193 65          70          75          80
196 Gln Thr Ala Leu Gln Pro Ala Leu Lys Phe Asn Gly Gly Gly His Ile
197          85          90          95
200 Asn His Ser Ile Phe Trp Thr Asn Leu Ser Pro Asn Gly Gly Gly Glu
201          100         105         110
204 Pro Lys Gly Glu Leu Leu Glu Ala Ile Lys Arg Asp Phe Gly Ser Phe
205          115         120         125
208 Asp Lys Phe Lys Glu Lys Leu Thr Ala Ala Ser Val Gly Val Gln Gly
209          130         135         140
212 Ser Gly Trp Gly Trp Leu Gly Phe Asn Lys Glu Arg Gly His Leu Gln
213 145          150         155         160
216 Ile Ala Ala Cys Pro Asn Gln Asp Pro Leu Gln Gly Thr Thr Gly Leu
217          165         170         175
220 Ile Pro Leu Leu Gly Ile Asp Val Trp Glu His Ala Tyr Tyr Leu Gln
221          180         185         190
224 Tyr Lys Asn Val Arg Pro Asp Tyr Leu Lys Ala Ile Trp Asn Val Ile
225          195         200         205

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228 Asn Trp Glu Asn Val Thr Glu Arg Tyr Met Ala Cys Lys Lys
229      210                      215                      220
232 <210> SEQ ID NO: 14
233 <211> LENGTH: 976
234 <212> TYPE: DNA
235 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 14
238 gcgggcggcg caggagcggc actcgtggct gtggtggctt cggcagcggc ttcagcagat      60
240 cggcggcatc agcggtagca ccagcactag cagcatgttg agccgggcag tgtgcggcac      120
242 cagcaggcag ctggctccgg ctttggggta tctgggctcc aggcagaagc acagcctccc      180
244 cgacctgccc tacgactacg gcgccctgga acctcacatc aacgcgcaga tcatgcagct      240
246 gcaccacagc aagcaccacg cggcctacgt gaacaacctg aacgtcaccg aggagaagta      300
248 ccaggaggcg ttggccaagg gagatgttac agcccagaca gctcttcagc ctgcactgaa      360
250 gttcaatggt ggtggtcata tcaatcatag cattttctgg acaaacctca gccctaacgg      420
252 tgggtggagaa cccaaagggg agttgctgga agccatcaaa cgtgactttg gttcctttga      480
254 caagttaaag gagaagctga cggctgcacg tggtggtgtc caaggctcag gttgggggtg      540
256 gcttggtttc aataaggaac ggggacactt acaaattgct gcttgtccaa atcaggatcc      600
258 actgcaagga acaacaggcc ttattccact gctggggatt gatgtgtggg agcacgctta      660
260 ctaccttcag tataaaaatg tcaggcctga ttatctaaaa gctatttgga atgtaatcaa      720
262 ctggggagaat gtaactgaaa gatacatggc ttgcaaaaag taaaccacga tcgttatgct      780
264 gagtatgtta agctctttat gactgttttt gtagtggtat agagtactgc agaatacagt      840
266 aagctgctct attgtagcat ttcttgatgt tgcttagtca cttatttcat aaacaactta      900
268 atgttctgaa taatttctta ctaaacattt tgttattggg caagtgattg aaaatagtaa      960
270 atgctttgtg tgattg
273 <210> SEQ ID NO: 15
274 <211> LENGTH: 497
275 <212> TYPE: PRT
276 <213> ORGANISM: Homo sapiens
278 <400> SEQUENCE: 15
280 Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp Tyr Asp Leu Ile
281 1      5      10      15
284 Ile Ile Gly Gly Ser Gly Gly Leu Ala Ala Ala Lys Glu Ala Ala
285      20      25      30
288 Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val Thr Pro Thr Pro
289      35      40      45
292 Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys
293      50      55      60
296 Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gln Ala Leu
297 65      70      75      80
300 Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu Thr Val Lys His
301      85      90      95
304 Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His Ile Gly Ser Leu
305      100     105     110
308 Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu
309      115     120     125
312 Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn
313      130     135     140
316 Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala
317 145     150     155     160

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320 Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr
321          165          170          175
324 Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
325          180          185          190
328 Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
329          195          200          205
332 Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
333          210          215          220
336 Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
337 225          230          235          240
340 Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
341          245          250          255
344 Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
345          260          265          270
348 Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr Asn Thr Val Met
349          275          280          285
352 Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile Gly Leu Glu Thr
353          290          295          300
356 Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp
357 305          310          315          320
360 Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
361          325          330          335
364 Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
365          340          345          350
368 Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
369          355          360          365
372 Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
373          370          375          380
376 Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
377 385          390          395          400
380 Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
381          405          410          415
384 Asp Asn Asn Lys Cys Tyr Ala Lys Ile Cys Asn Thr Lys Asp Asn
385          420          425          430
388 Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
389          435          440          445
392 Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu Thr Lys Lys Gln
393          450          455          460
396 Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
397 465          470          475          480
400 Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile Leu Gln Ala Gly
401          485          490          495
404 Cys
408 <210> SEQ ID NO: 16
409 <211> LENGTH: 1314
410 <212> TYPE: DNA
411 <213> ORGANISM: Homo sapiens
413 <400> SEQUENCE: 16
414 gaattcgggt ggagtcctga aggagggcct gatgtcttca tcattctcaa attcttgtaa

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60

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,19,20,21,22

VERIFICATION SUMMARY

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